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REMARKS

An Excess Claim Fee Payment Letter is submitted herewith for one excess total claim and one excess independent claim.

Claims 1-30 are all the claims presently pending in the application. Claims 1 and 24 have been amended to more particularly define the invention. Claim 30 has been added to claim additional features of the claimed invention.

It is noted that the claim amendments are made only for more particularly pointing out the invention, and not for distinguishing the invention over the prior art, narrowing the claims or for any statutory requirements of patentability. Further, Applicant specifically states that no amendment to any claim herein should be construed as a disclaimer of any interest in or right to an equivalent of any element or feature of the amended claim.

Claims 16-20, 22 and 23 stand rejected under 35 U.S.C. §101 allegedly because the claimed invention is directed to non-statutory algorithm type subject matter.

Claims 1-6, 9-11, 13-21, 23 and 27-29 stand rejected under 35 U.S.C. §102(b) as being allegedly anticipated by Nishikawa ("An Integrated Analysis and Database System for Full-Length cDNA", *Genome Informatics*, 11:12-23 (2000)). Claims 1-29 stand rejected under 35 U.S.C. §103(a) as allegedly unpatentable over Nishikawa taken with Rigoutsos, et al. (COMBINATORIAL PATTERN DISCOVERY IN BIOLOGICAL SEQUENCES: THE TEIRESIAS ALGORITHM, *BIOINFORMATICS*, Vol. 14, No. 1, Pages 55-67, 1998) (hereinafter, "the Teiresias paper").

These rejections are respectfully traversed in the following discussion.

I. THE CLAIMED INVENTION

The claimed invention (e.g., as recited in claim 1) is directed to a system for identifying genes. The system includes a pattern database comprising patterns of amino acids, and an input device for inputting a DNA sequence.

Importantly, the system further includes a processor which translates an open reading

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frame (ORF) of the DNA sequence into an amino acid translation, and locates in the amino acid translation occurrences of the patterns from the pattern database to determine whether the open reading frame includes a putative gene in the DNA sequence.

Conventional systems for identifying genes (e.g., putative genes) are either based on the use the statistics of DNA sequences, or the use of similarity searches to determine gene locations (Application at page 2, lines 7-22). However, these conventional methods have various problems which prevent them from efficiently identifying genes in a given DNA sequence (Application at page 3, line 19-page 4, line 21).

The claimed invention, on the other hand, includes a processor which translates an open reading frame (ORF) of the DNA sequence into an amino acid translation, and locates in the amino acid translation occurrences of the patterns from the pattern database to determine whether the open reading frame includes a putative gene in the DNA sequence (Application at Figure 1; page 5, lines 4-11). The claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

II. THE 35 USC §101 REJECTION

Claims 16-20, 22 and 23 stand rejected under 35 U.S.C. §101 because the claimed invention is directed to non-statutory algorithm type subject matter. Applicant submits, however, that these claims are clearly statutory subject matter and patentable.

Indeed, the Examiner again surprisingly attempts to support his allegations by referring to MPEP § 2106 (IV)(B)(2)(b), part ii, and stating that "a process that merely performs a purely mathematical algorithm is nonstatutory despite the fact that it might inherently have some usefulness" (Office Action at page 3).

However, Applicant would again point out to the Examiner that **MPEP § 2106 (IV)(B)(2)(b) covers only "Statutory Process Claims"**. Again, claims 16 and 23 are not directed to processes but are instead directed to a "method of identifying genes" and a

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"programmable storage medium", respectively.

Specifically, claim 23 is directed to a *"programmable storage medium tangibly embodying a program of machine-readable instructions executable by a digital processing apparatus to perform a method for identifying genes"*. Thus, claim 23 is not directed to a "process" and therefore, is not covered by MPEP § 2106 (IV)(B)(2)(b). Indeed, Applicant would direct the Examiner to MPEP § 2106 (IV)(B)(1)(a) which states:

"a claimed computer-readable medium encoded with a computer program is a computer element which defines structural and functional interrelationships between the computer program and the rest of the computer which permit the computer program's functionality to be realized, and is thus statutory".

Thus, MPEP § 2106 (IV)(B)(2)(b) clearly does not apply to the programmable storage medium defined in claim 23.

Moreover, with respect at least to claim 23, Applicant would direct the Examiner to MPEP § 2106 (IV)(B)(2)(a) which is entitled "Statutory Product Claims" and states "[i]f a claim defines a useful machine or manufacture by identifying the physical structure of the machine or manufacture in terms of its hardware or hardware and software combination, it defines a statutory product" (emphasis added) (citing *In Re Lowry*, 32 F.3d 1579 at 1583, and *In Re Warmerdam*, 33 F.3d 1354 at 1361-1362).

Further, with respect to claim 16, Applicant would point out that MPEP § 2106 (IV)(B)(2)(b)(ii) on which the Examiner relies, addresses only "Computer-Related Processes". Specifically, this section deals only with activity (e.g., manipulation of data or "number crunching") that is performed within a computer.

While claim 16 is directed to a "method of identifying genes", the claim **nowhere recites the term "computer"**. That is, this claim is not necessarily computer-related and certainly is not necessarily limited to activity that is performed within a computer. Thus, MPEP § 2106 (IV)(B)(2)(b)(ii) clearly does not apply to the method defined in claim 16.

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Again, Applicant would point out that a claim may be said to define statutory subject matter "when the machine, as claimed, produces a concrete, tangible and useful result" (*State Street Bank and Trust Co. v. Signature Financial Group, Inc.*, 149 F.3d 1368, 1374 (Fed. Cir. 1998)). In the present case, the claimed invention (e.g., as recited in claim 1) includes "*a processor which locates a pattern from said pattern database in said DNA sequence to identify a putative gene in said DNA sequence*". That is, in this exemplary embodiment, the processor may access the pattern database, and may locate a pattern from the pattern database in the DNA sequence (which was input by the input device) to identify a putative gene. The Applicant is puzzled how the Examiner can suggest that this is not a concrete, tangible and useful result, as required by *State Street Bank*. Clearly, the Examiner is incorrect, and the claims clearly define patentable subject matter.

In view of the foregoing, the Examiner is respectfully requested to reconsider and withdraw this rejection.

III. THE ALLEGED PRIOR ART REFERENCES

A. Nishikawa

The Examiner alleges that the Nishikawa teaches the claimed invention of claims 1-6, 9-11, 13-21, 23 and 27-29. Applicant submits, however, that there are elements of the claimed invention which are neither taught nor suggested by Nishikawa.

However, contrary to the Examiner's allegations, Nishikawa does not teach or suggest "*a processor which: translates an open reading frame (ORF) of said DNA sequence into an amino acid translation; and locates in said amino acid translation occurrences of said patterns from said pattern database to determine whether said open reading frame includes a putative gene in said DNA sequence*", as recited, for example, in claim 1, and similarly recited in claims 16, 23 and 29.

As noted above, unlike conventional systems for identifying genes (e.g., putative genes) which are either based on the use of the statistics of DNA sequences, or the use of similarity

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searches to determine gene locations, the claimed invention includes a processor which translates an open reading frame (ORF) of the DNA sequence into an amino acid translation, and locates in the amino acid translation occurrences of the patterns from the pattern database to determine whether the open reading frame includes a putative gene in the DNA sequence (Application at Figure 1; page 5, lines 4-11). The claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

Clearly, these features are not taught or suggested by the Nishikawa. Indeed, Nishikawa is merely directed to an annotation and database system for full-length cDNA sequences. Nowhere does Nishikawa teach or suggest locating in an amino acid translation of an ORF of a DNA sequence occurrences of patterns (e.g., biologically significant patterns) from pattern database to determine whether the open reading frame includes a putative gene.

Indeed, Nishikawa merely states that "Blastx[12] was used as a similarity search program". The Examiner then surprisingly attempts to improperly rely on **two secondary references** (e.g. Altschul et al. and Baxeavanis et al.) to supports his allegation that Nishikawa **anticipates** the claimed invention. The Examiner is clearly incorrect.

Indeed, contrary to the Examiner's allegations, Blastx is not used to locate in an amino acid translation of an ORF of a DNA sequence occurrences of patterns (e.g., biologically significant patterns) from pattern database to determine whether the open reading frame includes a putative gene (e.g., see Alschul at Abstract). In fact, Nishikawa merely **aligns a cDNA sequence with an amino acid sequence** (Nishikawa at Section 2.3.1 a) not to locate a putative gene, but to develop a database of full-length cDNA sequences. Applicant would point out that a "pattern" such as in the claimed invention is not merely an amino acid sequence but may be defined as a "pattern" (e.g., of amino acids) which may be discovered, for example, in a protein sequence.

Nowhere does either Nishikawa or Blastx even teach or suggest discovering patterns (In fact, Applicant would point out that the Examiner even concedes that Nishikawa does not teach

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or suggest a "pattern discovery algorithm" on page 7 in the Office Action). Thus, these reference certainly do not teach or suggest **locating occurrences of such patterns** in an amino acid translation of an ORF of a DNA sequence.

Therefore, Applicant submits that there are elements of the claimed invention that are not taught or suggest by Nishikawa. Therefore, the Examiner is respectfully requested to withdraw this rejection.

B. The Teiresias Paper (Rigoutsos et al.)

The Examiner alleges that Nishikawa would have been combined with the Teiresias paper to form the claimed invention of claims 1-29. Applicant submits, however, that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention.

Applicant respectfully submits that these references would not have been combined as alleged by the Examiner. Indeed, these references are completely unrelated, and no person of ordinary skill in the art would have considered combining these disparate references, absent impermissible hindsight.

In fact, these references clearly do not teach or suggest their combination. Therefore, Applicant respectfully submits that one of ordinary skill in the art would not have been so motivated to combine the references as alleged by the Examiner. Therefore, the Examiner has failed to make a prima facie case of obviousness.

Indeed, Applicant would point out that the Examiner expressly concedes that the Teiresias paper teaches the shortcomings of Nishikawa et al. (Office Action at page 8).

Morover, neither Nishikawa, nor the Teiresias paper, nor any alleged combination thereof teaches or suggests However, contrary to the Examiner's allegations, Nishikawa does not teach or suggest *"a processor which: translates an open reading frame (ORF) of said DNA sequence into an amino acid translation; and locates in said amino acid translation occurrences of said patterns from said pattern database to determine whether said open reading frame includes a*

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putative gene in said DNA sequence", as recited, for example, in claim 1, and similarly recited in claims 16, 23 and 29.

Clearly, these features are not taught or suggested by the Teiresias paper. Indeed, as previously pointed out to the Examiner, the Teiresias paper discloses an algorithm (e.g., the Teiresias algorithm) for **discovering** in a biological sequence. In contrast, the claimed invention may **use such patterns which have already been discovered** using the Teiresias algorithm (as disclosed by the Teiresias paper) to identify genes in a DNA sequence.

That is, the Teiresias paper was directed to "pattern discovery", whereas the claimed invention may be considered to be directed to gene identification (e.g., "gene discovery") which involves locating patterns (which have already been discovered) in a DNA sequence. This is completely different than the pattern discovery method disclosed in the Teiresias paper. Indeed, nowhere is gene identification (e.g., "gene discovery") taught or suggested in the Teiresias paper.

Therefore, Applicant submits that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.

IV. FORMAL MATTERS AND CONCLUSION

In view of the foregoing, Applicant submits that claims 1-30, all the claims presently pending in the application, are patentably distinct over the prior art of record and are in condition for allowance. The Examiner is respectfully requested to pass the above application to issue at the earliest possible time.

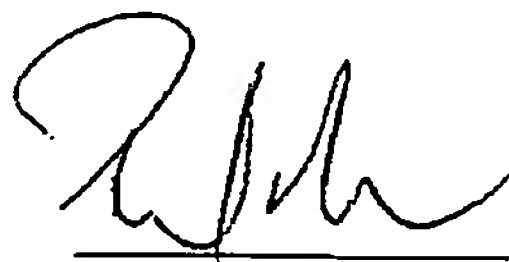
Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at the local telephone number listed below to discuss any other changes deemed necessary in a telephonic or personal interview.

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The Commissioner is hereby authorized to charge any deficiency in fees or to credit any overpayment in fees to Assignee's Deposit Account No. 50-0510.

Respectfully Submitted,

Date: 5/13/05

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CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that the foregoing Amendment was filed by facsimile with the United States Patent and Trademark Office, Examiner C. Dune Ly, Group Art Unit # 1631 at fax number (703) 872-9306 this ~~17~~ 13th day of May, 2004.



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